

Applicants: Christopher C. Fraser (as amended)
Serial No.: 09/766,511 Filed: January 19, 2001
Title: Nucleic acids encoding Tango 405 and functional fragments and uses thereof (as amended)

Atty/Agent: Mario Cloutier Attorney Docket No.: MPI00-537OMNIRCEM

Replacement Figure Sheet 1 of 39

Hum. Mur.	10 20 30 40 50 60 70 Hum. MRRQPAKVAALLLGLLLECTEAKKHCWYFEGLYPTYYICRSYEDCCGSRCCVRALSIQRLWYFWFLLMMG : : : : : : : : : : : : : : : : :	20 LLECTEAKKHC :.:::::::: LVECTEAKKHC	30 WYFEGLYPTYN :::::::::: WYFEGLYPTYN 30	40 IICRSYEDCCC ::::::::::::::::::::::::::::::::::	50 SSRCCVRALSI ::::::::::::::::::::::::::::::::::::	20 30 40 50 70 70 70 50 60 70 70 10 10 10 10 10 10 10 10 10 10 10 10 10	70 IMG :: IMG 70
Hum. Mur.	80 VLFCCGAGFFIRRRM ::::::::::::::::::::::::::::::::::	90 YPPPLIEEPAF ::::::::: YPPPLIEEPTF 90	100 NVSYTROPPNE:::::::::::::::::::::::::::::::::::	110 GPGAQQPGPI .:::::::	120 PYYTDPGGPGN:::::::::::::::::::::::::::::::::	90 100 110 140 YPPPLIEEPAFNVSYTRQPPNPGPGAQQPGPPYYTDPGGPGMNPVGNSMAMAFQV ::::::::::::::::::::::::::::::::::::	140 FQV ::: FQV 140
Hum. Mur.	150 PPNSPQGSVACPPPP ::::::::::: QPNSPHGGTTYPPPP	160 170 AYCNTPPPPYEQVVKAK ::::::::::::::::::::::::::::::::::	170 QVVKAK :::::: QVVKDK 170				

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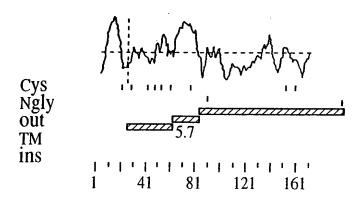


Fig. 1B

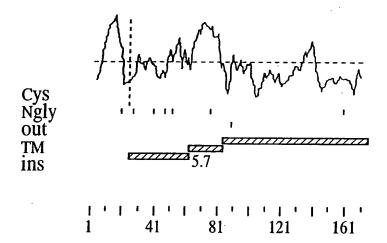
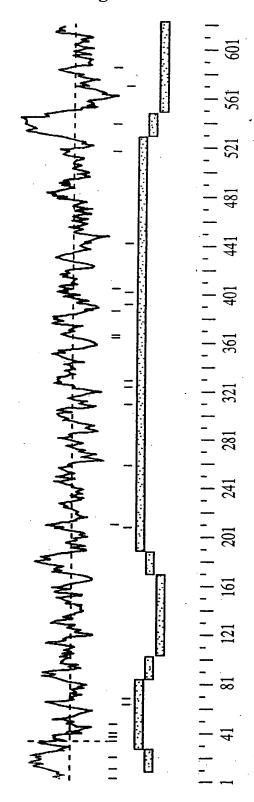


Fig. 1C

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20 30 40 50 60 AILNKVAPQACPAQCS-CSGSTVDCHGLALRSVPRNIPRNTERLDLNG .:.: .:: ::::::::::::::::::::::::::::	90 100 110 120 130 RVLQLMENKISTIERGAFQDLKELERLRLNRNHLQLFPELLFLGTAKLYRLDL .: .: .: .: .: .: .: .: .: .: .: .: .: .	200 SFNHMPKLRTF :: TF	270 MAPSCSVLHCP
50 IGLALRSVPRNI .:.: :::: NLGLSSIPKNF	120 .NHLQLFPELLFLGTA. .::: HLYFLFLNNN. 110	190 NNNNITRLSVA . : .: : . QRNRLTVLGSG	230 240 250 260 270 DWLRQRPRVGLYTQCMGPSHLRGHNVAEVQKREFVCSGHQSFMAPSCSVLHCP ::. ::VGMVA
40 S-CSGSTVDCH ::: .:: QLCTGRQINCR	110 LKELERLRLNR : . LR	180 RALRDLEVLTL .: :.: NDLVSVQYLNL 160	250 LRGHNVAEVQK :: VA
30 VAPQACPAQC:. : -EILGCSSVC 30	100 STIERGAFQD: SYVYPKAFVQ: 100	170 SISCIEDGAFI :.: :.: SVSFVPRGVFI	240 .YTQCMGPSH1
20 .AILNK' .TCYLLLLLHK. 20	90 *VLQLMENKI: .: :: /ALYLDNSNII	160 DIKNLQLDYNÇ :::::::::::::::::::::::::::::::::::	230 WLRQRPRVGLY ::.
10 Slit MRGVGWQMLSLSLGLVL? : : : : :: 325 MCGLQFSLPCLRLFLVVT	70 80 90 100 Slit NNITRITKTDFAGLRHLRVLQLMENKISTIERGAFQDLKE ::::::::::::::::::::::::::::::::::::	140 150 200 Slit SENQIQAIPRKAFRGAVDIKNLQLDYNQISCIEDGAFRALRDLEVLTLNNNNITRLSVASFNHMPKLRTF : :::::::::::::::::::::::::::::::::	210 220 Slit RLHSNNLYCDCHLAWLSD 325
325	Slit 325	Slit 325	Slit 325

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O APDAF	1 - -	J IIAKG) AKEQY 	ATGIF
340 NQISELA	: · : O	410 YDNKLQT	480 KKFRCSAI	0 LNNNEFTVLEA' .:.:::
280 330 340 340 320 320 330 340 AACTCSNNIVDCRGKGLTEIPTNLPETITEIRLEQNTIKVIPPGAFSPYKKLRRIDLSNNQISELAPDAF	:: .::::: LRILDLSNNNI 190	370 380 400 410 TELPKSLFEGLFSLQLLLLINANKINCLRVDAFQDLHNLNLLSLYDNKLQTIAKG .: SESGFQHLENLACL	440 450 460 470 480 PFICDCHLKWLADYLHTNPIETSGARCTSPRRLANKRIGQIKSKKFRCSAKEQY ::::	510 520 530 540 550 FADLACPEKCRCEGTTVDCSNQKLNKIPEHIPQYTAELRLNNNEFTVLEATGIF .:.:::: SNAFEVLKS
320 KVIPPGAFSPY		390 KINCLRVDAFQ :: SGFQ	460 GARCTSPRRL	530 QKLNKIPEHIPQ .:.:: -NLTKVP
310 TEIRLEONTIF		380 SLQLLLLNANF	450 ADYLHTNPIETS ::::	520 CEGTTVDCSNQK
300 SIPTNLPETI		370 JPKSLFEGLF:	440 CDCHLKWLAI	2. 510 LACPEKCRCI
290 IVDCRGKGLTE		360 JVLYGNKITEI ::: ISE-	430 TMHLAQNPF1	500 SKLSGDCFAL
280 AACTCSNNI	 	350 360 QGLRSLNSLVLYGNKI:::::	420 430 TFSPLRAIQTMHLAQNI	490 500 FIPGTEDYRSKLSGDC
Slit	325	Slit 325	Slit 325	Slit 325

Fig. 2(

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			_	
620 RSNRITCVGND	:: : : KNSRIRNVTRD	690 IVTGNPRCQKP	760 NDVTELYLDGN	LNSD 830 GLKSLRLLSLH :::: -LKPL
580 590 600 600 610 620 610 620 DIEEGAFEGASGVNEILTSNRLENVQHKMFKGLESLKTLMLRSNRITCVGND	:::::: :::::::::::::::::::::::::::::::	650 670 680 690 ITTVAPGAFDTLHSLSTLNLLANPFNCNCYLAWLGEWLRKKRIVTGNPRCQKP ::: 290	720 730 740 750 760 CDDGNDDNSCSPLSRCPTECTCLDTVVRCSNKGLKVLPKGIPRDVTELYLDGN	
600 RLENVQHKMFI	: E	670 LANPFNCNCYLZ ::: LEN2	740 CLDTVVRCSNF	810 2LLTLILSYNF : .: ::: 330
590 GVNEILLTSNI		660 LHSLSTLNLLAN ::: LEN 290	730 PLSRCPTECTO	790 800 810 820 IDLSNNRISTLSNQSFSNM-TQLLTLILSYNRLRCIPPRTF . : .: .: .: .: .: .: .: .: .: .: .: .:
580 IEEGAFEGAS	::. IQPFA	650 TTVAPGAFDT	720 DDGNDDNSCSI	790 DLSNNRISTLS:::::KLDRNRIISII
570 INFSNNKITD	:::: : ::. LRRLSLSHNPIEAIQ- 230 240	630 640 SFIGLSSVRLLSLYDNQI ::::::.:	700 YFLKEIPIQDVAIQDFTC	780 LSNYKHLTLII : .: 300
560 570 Slit KKLPQLRKINFSNNKIT				770 t QFTLVPKEI :::. 5 TFSLL
Slit	325	Slit 325	Slit	325 325

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			,
900 DKLLLTTPSK 	970 NPCKHGGTCH : .:: -PSMRG	1040 EEKLDFCAQD	1110 EGYSGLFCEF
890 IARCAGPGEMA	960 DCDVPIHACIS : : -CQNP	1030 LCPPEYTGELC	1070 1080 1090 1100 1110 KCDCTPGYVGEHCDIDFDDCQDNKCKNGAHCTDAVNGYTCICPEGYSGLFCEF :
880 IVKSEYKEPG . :	950 TCPYGFKGQ	1020 : : :V	1090 KCKNGAHCTI
870 CDCNMQWLSDWV :.: :::. CNCKLGLRDWI	940 NSDPVDFYRC :	1010 DNDCENNSTCV: ::: NITNCV:	1080 DIDFDDCQDN
50 860 870 SALSHLAIGANPLYCDCNMQWLSDWVKS: :.::::::::::::::::::::::::::::::::::	930 SNPCKNDGTC	1000 ACEVNVDDCE	1070 TPGYVGEHCI
850 FNDLSALSHI :::::	920 IILAKCNPCLS : II	990 :: :	1060 LTPKGFKCDC
840 850 870 880 890 900 Slit GNDISVVPEGAFNDLSALSHLAIGANPLYCDCNMQWLSDWVKSEYKEPGIARCAGPGEMADKLLTTPSK : : : : : : : : : : : : : : : : : : :	910 920 930 940 950 960 970 KFTCQGPVDVNILAKCNPCLSNPCKNDGTCNSDPVDFYRCTCPYGFKGQDCDVPIHACISNPCKHGGTCH	980 1000 1010 1020 1030 1040 LKEGEEDGFWCICADGFEGENCEVNVDDCEDNDCENNSTCVDGINNYTCLCPPEYTGELCEEKLDFCAQD:RALRYI	1050 1060 LNPCQHDSKCILTPKGF
Slit 325	Slit 325	Slit 325	Slit 325

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		replacemen	it Figure Sheet	8 01 39
0 1140 1150 1160 1170 1180 CQNGAQCIVRINEPICQCLPGYQGEKCEKLVSVNFINKESYLQIPSAKVRPQTN	:: MMAWHKV	1190 1200 1250 1250 1250 1250 1250 1250 125	1260 1270 1280 1290 1300 1310 1320 LSVDGGNPKIITNLSKQSTLNFDSPLYVGGMPGKSNVASLRQAPGQNGTSFHGCIRNLYINSELQDFQKV :: ::::::::::::::::::::::::::::::::::	1350 1360 1370 1380 1390 CAHGTCQPSSQAGFTCECQEGWMGPLCDQRTNDPCLGNKCVHGTCLPINAFSY FFIL
1170 NFINKESYL	:: .: .: :: .: .: .: .: .:: .:	1240 SVETINDGNFH QENAFGNP-LE 470	1310 SFHGCIRNL:	1380 IDPCLGNKCVI
1160)GEKCEKLVS1	: SI 420	1230 SSHPASAIYSV ::	1300 ILRQAPGQNGT	1370 MGPLCDQRTN
1150 EPICQCLPGY(1220 YRGRVRASYDTC : .: FWERIPTS	1290 GGMPGKSNVAS .:.: SMSGKTSLI-	1360 .: :-F
1140 IGAQCIVRINI	· : · ·VVK	200 1210 LYKGDKDHIAVELYF : :	1280 STLNFDSPLYVG :.: : SALPNDAA	1350 HGTCQPSSQA
1130 SPCDNFDCQN		1200 DSGILLYKGD : SPLENTE	1270 IITNLSKQST . :: ::: -TLNLEKNSA 500	1340 EPCHKKV
1120 1130 : SPPMVLPRTSPCDNFDC	 5VSRAWA-			1330 1340 PMQTGILPGCEPCHKKV ::: NEAFDILLA
Slit	325	Slit 325	Slit 325 49	Slit 325

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	1400	1410	1420	1430	1440	1450	1460	
lit	SCKCLEGHGGV	COEEEDL	lit SCKCLEGHGGVLCDEEEDLFNPCQAIKCKHGKCRLSGLGQPYCECSSGYTGDSCDREISCRGERIRDYYQ	KCRLSGLGQP	YCECSSGYTG	DSCDREIS	CRGERIRDYYQ	
	••			•	•	••		
325	325 ACV	TITI	IIFLIYKVVQFKQKLKA	KLKA	SENS	- 1	RENRL-EYY-	
	540		550		560		570	
	1470	1480	1490	1500	1510	1520		
lit	KQQGYAACQTI	K-KVSRLE	Lit KQQGYAACQTTK-KVSRLECRGGCAGGQCCGPLRSKRRKYSFECTDGSSFVDEVEKVVKCGCTRCVS	PLRSKRRKYS	FECTDGSSFV	DEVEKVVK	CGCTRCVS	
			•••••••••••••••••••••••••••••••••••••••	••	••	•••	•	
325 .	SFYQSA	RYNVTASI	SFYQSARYNVTASICNTSPNSLESPGLEQIRLHK	LEQIRLHK	VIQ	QIVPENEAQVI-LFEHSAL	-LFEHSAL	
		280	590	009		610	620	
				(
				F19. 2C				

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70 ATATTATT	140 16CGCGGT	210 AGATGCGC	280 GCACCGC :::
60 CCTTGTTCC	 130 CTCAGACAC	200 GGCGGGGAAZ	270 3AACAAGGTG
50 SGCTCTACTG	120 3GCACTGGGC	190 3GAAGGAGGC	260 GGCGATCCT(
40 GCCTGAGTG	110	180 TGCCGGCGAC	250 GGTTAGTGCT
30 GGAGGCGTGI	100 TGGGTTGCTA	170 AAGCCCCCAG	230 240 250 260 270 280 GCTGTCCCTGTCGCTGGGGGTTAGTGCTGGCGATCCTGAACAAGGTGGCACCGC ::: :: :: ::
20 GAGGCGGTG	90 CCTGGCACTC	160 AAGCTAAAGA	230 GATGCTGTCC
10 20 40 50 70 Slit CAGAGCAGGGTGGGAGGCGTGTGCCTGAGTGGGCTCTACTGCCTTGTTCCATATTATT		150 160 170 180 190 200 210 TCCCTCGGAGCAGCAAGCTAAAGAAGCCCCCCAGTGCCGGCGGCGGGGGAAGATGCGC	220 GGCGTTGGCTGGCAGAT
Slit		325 Slit 7	Slit (

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350 CAGCGT :::	420 'ACGAAG	490 CCATTGAAA ::.:: CCTTTA 50	560 CTGTTTCC ::::
340 TGGCGCTGCG	410 CACAAGAATT	480 ATTAGCACCA ::-	550 ACCTTCAGCT
330 :TGTCACGGGC' ::: CACG	400 GAAATAACAT(470 TTATGGAGAATAAG? :::.:: TTTAAAAAGAAAA	540 TTAAACAGAAATCAC ::::: :: TTAATAATACG- 80
320 3CACAGTGGAC	390 GATTTAAATG	460 470 GTTCTTCAGCTTATGGAGAATAA:::::::::::::::::	530 ACTGCGTTTA :::
310 TGCTCGGGCAC	380 CCGAGAGACTC	450 ICTAAGAGTIC: :::: GIIC:	520 SAACTAGAGAGA :.:::::-: -AGCT-GAGTG-
300 GCAGTGCTCT	370 CCCCGCAACA	440 GTCTTAGACA'	510 CCAGGATCTTAAA(:::::: -CTGAATC
290 340 350 350 350 350 340 350 340 350 340 350 340 350 340 350 340 350 340 350 340 350 340 350 340 350 340 350 350 340 350 350 350 350 350 350 350 350 350 35	360 370 380 420 GCCCAGGAATATCCCCCCCCAACACACCGAGAGACTGGATTTAAATGGAAATAACATCACAAGAATTACGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGA	430 440 450 460 470 480 490 ACAGATTTTGCTGGTCTTAGAGTTCTTCAGCTTATGGAGAATAAGATTAGCACCATTGAAA ::::::::::::::::::::::::::::::::	500 510 520 530 540 550 56 GAGGAGCATTCCAGGATCTTAAAGAACTAGAGACTGCGTTTAAACAGAAATCACCTTCAGCTGTTTC :::::::::::::::::::::::::::::::
Slit 325	Slit 325	Slit 325	slit (325 .

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		кері	accincia		, ure s	meet	12 01		
630 3CAATC	 - -	700 CTGTA	GTT 150	770	ACTAG		840 TGTAT	· · E	200
620 CCAAATTCAGG	ACAGA-AAATCCAAGAACAGG 120	690 AACCAGATCAG	·	760	ATAACAACATT :		830 FTCAAACAACC		
610 620 CTCAGTGAAAACCAAATTCA	-ACAGA-AAAT(120	680 AACTGGATTACZ	14	750	ACICICAACAA 	170.	790 830 810 820 830 840 TCAACCATATGCCTAAACTTAGGACTTTCGACTGCATTCAAACAACCTGTAT	· · · · · · · · · · · · · · · · · · ·	+ +
600 CAGGCTTGATO	! ! ! !	670 AAAAATTTGC?	-GATATGTG	740			810 ACTTAGGACTI		1 i)
590 CGAAGCTATACAGG	-CCAATTCTGATCTGA- 100 110	660 AGTTGACATA	 	730	910000EDED		800 ATATGCCTAA	:. TGTTA	190
580 CTTGGGACTG	5,T.T.C	650 TCCGTGGGGC		720			790 AGTTTCAACC	CIGGITGITACCIGITA-	180 1
Slit TGAGTTGCTGTTTCTTGGGACTGCGAAGCTATACAGGCTTGATCTCAGTGAAAACCAAATTCAGGCAATC	06 .TT.,	640 650 660 670 680 690 700 CCAAGGAAAATTTGCAACTGGATTACAACCAGATCAGCTGTA GCTTGACATCAGCTGTA 690 700		710	**************************************		780 ACTTTCTGTGGCAAGTT	::::::::::::::::::::::::::::::::::::::	Н
Slit	372	Slit	325		325		Slit	325	

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910 CTCAGT :: :	980 TCTGCAGTGG :::::: TCTGCACTGG 250	1050 AACAAT	1120 AAATAC :::
900 STTGGTCTGTACACTCAG ::::::::::::::	930 940 950 960 970 980 CCTGAGAGGCCATAATGTAGCCGAGGTTCAAAAACGAGAATTTGTCTGCAGTGG ::: ::: :: :: :: :: :: :: :: :: :: :: :	1000 1010 1020 1030 1040 1050 GCTCCTTCTTGTAGTGTTTTGCACTGCCCTGCCGCCTGTACCTGTAGCAACAAT ::::::::::::::::::::::::::::::::	1070 1080 1090 1100 1110 1120 GGAAAGGTCTCACTGAGATCCCCCACAAATCTTCCAGAGACCATCACAGAAATAC . :: :: :: :: :: :::::::::::::::::::::
890 36CCTCGG .: IAC	960 CAAAAACC	1030 CTGCCGCC	1100 TCTTCCAGAGA : :::::::: TTTTCCTGAAA
880 STTCGCCAAAGGC ::::::	950 TAGCCGAGGT3 ::: -AGC	1020 TTGCACTGCC::::::::::::::::::::::::::::::	1090 TCCCCACAAA
870 TCCGACTGGC	940 3GCCATAATG1	1010 TTGTAGTGTT	1080 CTCACTGAGAT : :::: 'CCTAAGA-
860 GGCCTGGCTC .: AG	930 CACCTGAGAG	1000 TGGCTCCTTC	1070 TGGGAAAGGTCT .: .: :: AGTATTC-
850 860 870 880 890 900 910 Slit TGTGACTGCCACCTGGCTCTCCGACTGGCTTCGCCAAAGGCCTCGGGTTGGTCTGTACACTCAGT ::::::::::::::::::::::::::::::::::::	920 GTATGGGCCCCTCCCA ::::: GTTTGTC	990 TCACCAGTCATTTATG ::::::.: GAGACAAATTA- 260	1060 ATCGTAGACTGTCGTG :::::: CTTTCGAG
Slit 325	Slit 325	Slit 325	Slit 325

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			,
1190 TTAGACGAAT ::.:: AAAGT-GAAT 370	1260 GAATTCA ::::	1330 CTTACAGC ::.:: CTAACA	0 1400 CACAACTTGAA ::::::: CATCTATAT 460
70 1180 CATATAAAAAGCTTA :.::::::: CTTATATAAATGAAA	1250 ACGCTCTCT:::TC	1320 13 CTGTTTTCCTTACA ::::::::::::::::::::::::::::	1390 ATCTCCACA :: CA
1160 1170 1180 1190 1190 1190 1190 1190 1190 119	1240 TTCCAAGGACTAĞG :::::: AGGACTTC- 380	1280 1300 1310 1330 ATAAAATCACAGAACTCCCCAAAGTTTATTTGAAGGACTGTTTTCCTTACAGC ::::::::::::::::::::::::::::::::::	1350 1360 1370 1380 1390 1400 CAACAAGATAAACTGCCTTCGGGTAGATGCTTTTCAGGATCTCCACAACTTGAA ::::::::::::::::::::::::::::::::::
1160 CCTGGAGCTTT :::::	1230 CACCAGATGCT	1300 CCCAAAAGTT : : ATTG	0 TGCCTTCGGGTAGA ::::::
1150 GTCATCCCT	1220 CTGAACTTG	1290 CACAGAACTO ::: AGC	1360 ATAAACTGCC ::: GCC
1140 CACAATCAAA	1210 AATCAGATCT	1280 3AAATAAAAT	1350 FGCCAACAAG : ::::: F-CCAAAA
1130 1140 1150 1160 1170 1180 1190 GTTTGGAACAGAACAATCAAAGTCATCCTCCTGGAGCTTTCTCACCATATAAAAAGCTTAGACGAAT :::::::::::::::::::::::::::::::::::	1200 1250 1260 TGACCTGAGCAATAATCAGATCTCTGAACTTGCACCAGATGCTTTCCAAGGACTACGCTCTCTGAATTCA ::: TAACAGGACTTCATTCT	1270 Slit CTTGTCCTCTATGGAA ::::: 325 CTTGT	1340 Slit TCCTATTATTGAATGC : :: :.:: TTCTGTATGTATAT-C
Slit 325	Slit 325	Slit C : 325 C 390	Slit

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	Replacement	. Figure Sheet 1	(3 01 3)
1470 GGCCATT :	0 GGATTATCTCC :::::	1610 AAAGAATTGG :: ATTTATATTT	1680 GATTAT
1460 ACCTCTTCG : A	1530 GGCTAGCGGAT' :.::. GACTTTTA	1600 CAAACAAAA(:.:	1670 AGGTACAGAA
1450 GGGACCTTTTCA ::::: TTTCA 490	1520 ATCTCAAGTGGCTAG ::::::. AAGGGACTTT 520	560 1570 1580 1590 1600 1610 ACCAGTGGTGCCCCCCCCCCCCCCCCCCTGGCAAACAAATTGGGCCCAGTGGCAAACAAA	1660 AGTATTTCATTCC <i>F</i> :::::::: AGTATTTAAT
1440 CATCGCCAAG	1510 TGTGACTGCC? :	1580 GCACCAGCCCC	1650 TAAAGAACAGT ::: ::: GAGAGGAGT 580
1430 AGCTTCAGAC	1500 CCCTTTATT ::::	1570 GTGCCCGTT	630 1640 1650 AATTCCGTTGTTCAGCTAAAGAAC : ::::::::::::::::::::::::::::::::::
1420 CTATATGACAACA <i>i</i> ::::::: CTAAATAATAA 480	1490 TTTGGCCCAGAAC ::.:.:::: TTAGATCCTGGA- 510	1560 TTGAGACCAGTG	1630 :AAGAAATTCCG :.::::: :AGGTATCTT
1410 1420 1430 1440 1450 1460 1460 1470 CCTTCTCTCCCTATATGACAAGCTTCAGACCATCGCCAAGGGGACCTTTTCACCTCTTCGGGCCATT ::::::::::::::::::::::::::::::::::	1480 1490 1500 1510 1520 1530 1540 CAAACTATGCATTTGGCCCAGAACCCCTTTATTTGTGACTGCCATCTCCAAGTGGCTAGCGGATTATCTCC ::::::::::::::::::::::::::::::	1550 1 ATACCAACCCGATTGAG ::: GTA540	1620 1630 1680 1680 1680 1680 1680 1680 1680 168
Slit 325	Slit 325	Slit ATAC .:: 325 GTA-540	Slit 2

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1750 GGAACCA	 	1820 AGTTGCG	1890 ACGTAAA	1960 GTAAATG
1740 TCGCTGTGAA		1810 TACACTGCAG :::: CACTG 640	1880 TTCCTCAATT: :.::: TACCT	1950 AGCATCTGGT(::::: CTTCGG 680
1730 CTGAAAAGTG		1800 ACATTCCCCAG ::::.	1870 TTTAAGAAAC	910 1920 1930 1940 1950 1960 TAAGATCACAGATATTGAGGGGGGGGGCATTTGAAGGAGCATCTGGTGTAAATG
1720 CIGGCIIGC	 TCAG	1790 TCCCGGAGCA ::: GGAA	1860 CACAGGAATC .:: TGG	20 1930 ATATTGAGGAGGAGCA .:.:::: TTGTTGTATGGTTGCT
1710 CTTTGCGGAT	CAGTTCAG	1780 CTCAACAAAA ::::	1850 TGTTGGAAGC :::::: TTGGGAG- 650	1920 CACAGATATTGA .:.::.
1700 GTGGAGACTG		60 1770 1GCTCTAATCAAAG 1.:: .:::: TACTTAAATCTA	1840 GAATTTACCG	1910 ACAATAAGAT
1690 1700 1710 1720 1730 1740 1750 Slit CGATCAAAATTAAGTGGAGACTGCGATCTGGCTTGCCCTGAAAAGTGGCTGTGAAGGAACCA	-GATCTAGTTT 600	1760 1770 1780 1800 1810 1820 Slit CAGTAGATTGCTCTAATCAAAAATCCCGGAGCACATTCCCCAGTACACTGCAGAGTTGCG :.:: .::::::::::::::::::::::::::::::::	1830 1840 1850 1860 1870 1880 1890 TCTCAATAATAATGAATTTTACGGAAGCCACAGGAATCTTTAAGAAACTTCCTCAATTACGTAAA .:::::::::::::::::::::::::::::::::	1900 ATAAACTTTAGCAACAA
Slit	325	Slit 325	Slit 325	Slit 325

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		U	
2030 3CCTCAA : A	2100 FTCTGTG	2170 CATTCTT	2240 AGTGGCT :
2020 3GATTGGAAA	2090 FAGGACTCAG	2160 GATACTCTC	2230 GCTTGGTTGGGAGA ::::: :: GCTTGTTTGTAT
2010 3ATGTTCAAGO	2070 2080 GTGTGGGGAATGACAGTTTCAT .: : .: : : : : : : : : : : : : : : : :	2150 CAGGGGCATTI	2220 %TACCTGGCTT ::::
2000 IGCAGCATAAC	2070 TGTGGGGAATC:::::::::::::::::::::::::::::	2140 ACAGTTGCACC	2210 ACTGTAACTGC
1990 FTGGAAAATG1	2060 SAATAACCTG1 :::::::	2130 CCAAATTACTA	2200 AATCCTTTTAA :::::: AAACCTT
1980 ACGAGTAATCGT1 :::::: GATTTATC 690	2050 GAAGCAATCO	2120 GTATGATAA1	0 2190 2200 TAAACCTCTTGGCCAATCCTTT ::::::::::
1970 1980 2000 2010 2020 2030 Slit AAATACTTCTTACGAGATTTGGAAAATGTGCAGCATAAGATGTTCAAGGGATTGGAAAGCCTCAA :::::: :: ::::::::::::::::::::::::::	2040 2050 2070 2080 2100 Slit AACTTTGATGTGAATGACCTGTGTGGGGAATGACAGTTTCATAGGACTCAGTTCTGTG ::: 325 AACAATAAC-ATTTGAGGATATCAGAATCAG	2110 2120 2140 2150 2170 CGTTTGCTTTCTTGTATGATAATTACTACAGTTGCACCAGGGGCATTTGATACTCTCCATTCTT :::::GCTTTC	2180 2230 2240 TATCTACTCTAAACCTCTTGGCAATCCTTTTAACTGTAACTGCTACCTGGCTTGGTTGG
Slit 325	Slit 7	Slit (325	Slit 325

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2310 ACCCATC :: AC	2380 CCACTTTCTC :.:::: -CTTTGTCTC 840	2450 rctrgcc .::::::	2520 CAAGGAA
2260 2300 2310 GTCACGGGAAATCCTAGATGTCAAAAACCATACTTCCTGAAAGAAA	2370 TTGCTCCCCA:	2400 2410 2420 2430 2440 2450 TACTIGCTIGGATACAGTCGTCCGATGTAGCAACAGGGTTTTGAAGGTCTTGCC ::.:::::::::::::::::::::::::::::::::	2510 CACTGGTTCCC :::
2290 CCATACTTCC' ::::	2360 TGATGACAATAG' .:.:::: AGAAGACTTT	2430 FAGCAACAAG(:: CA	2500 GGAAACCAATTTAC :::: ATACC
2280 22 ATGTCAAAAACCATA .:::::::::-:	2350 SACGGAAATGA .:	410 2420 ATACAGTCGTCCGATG:::::::	2490 TCTGGATGGAA :::::: TCTGGAAT
2260 2270 GTCACGGGAAATCCTAG . :	2340 CACTTGTGAT(2410 FTGGATACAG :::::: AATACAG	2480 SAGAGTTGTA:
2260 TTGTCACGGG:::: TTAACAAA	2330 ATTCAGGACTTC ::::::: TTAAAAGICTT-	2400 TGTACTTGCTT ::. GCA- 860	2470 GAGATGTCAC
2250 Slit GAGAAAGAAGAATT ::::::::325 TAGGAAGTAATTT 770 780	2320 2330 2340 2350 2360 2370 2388 Slit CAGGATGTGGCCATTCACTTGTGATGATGATGATGATAGTTGCTCCCCACTTTCT	2390 GCTGTCCTACTGAATG : : : : : : : : :	2460 2470 2480 2500 2510 2520 GAAAGGTATTCCAAGAGTTGTATCTGGATGGAAACCAATTTACACTGGTTCCCAAGGAA ::::::::::::::::::::::::::::::
slit 325	Slit 325	Slit 325	Slit 325

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0 2590 TTCTAATCAGA : ::: : : - -TTTAGTGG 950	2660 CTCCTCG	2730 TGCCTGAA :.::: :: TACCTTAA 1050	0 2800 CTGTGATTGTA : ::: GATAATGAT 080
2580 ACGCTTTCT. : : TTT.	2650 AGATGTATTC ::. TAATGA	2720 TTCTGTTGT : :.: : TTAATTT 1040	2790 CTTTACTGTG :. GAT
540 2550 2560 2570 2580 2590 ITTAACACTTATAGACTTAAGTAACAACAGAATAAGCACGCTTTCTAATCAGA : ::::::::::::::::::::::::::::::::	2640 2650 AACCGTCTGAGATGTA ::::::	680 2690 2700 2710 2720 2730 AGTCTCTTCGATTACTTTCTCTACATGGAAATGACATTTCTGTTGTGCCTGAA :::::::::::::::::::::::::::::::::::	750 2760 2770 2780 2790 2800 TTCTGCATTATCACATCTAGCAATTGGAGCCAACCCTCTTTACTGTGATTGTA .:.::::::::::::::::::::::::::::::::::
2560 2570 TAAGTAACAACAGAATAAG :::::::::::::::::::::::::::::::	0 2630 TTAATTCTTAGTTAC :::::: TTTGATCTTAA	2700 TCTCTACATG(::.:.:: TCAGTTTG'	2770 TAGCAATTGG :::::: TAGCATT
2550 CTTATAGACT :: TTAGGA	2620 2630 TCACCTTAATTCTTAG ::::::::	2690 2700 TCGATTACTTTCTCTA(::.::::::::::::::::::::::::::::::::::	2760 CATTATCACATC :::: AATAAT
	2610 ACCCAGCTCC : A	2680 TAAAGTCTCT :.::: TTAAAT 1010	
2530 2540 Slit CTCTCCAACTACAACATTTAA ::::::.:: 325TCCTGAAAAATTCAAGAA- 910 920	2600 2630 2640 2650 2660 Slit GCTTCAGCAACATGACCCTCACCTTAATTCTTAGTTACAACCGTCTGAGATGTATTCCTCCTCG ::::::::::::::::::::::::::::	2670 CACCTTTGATGGATTAA :::::::: TTTAGAGAATTTA 1000	2740 2 Slit GGTGCTTTCAATGATCT : ::::325 GTTAGATAGAA
Slit 325	Slit 325	Slit 325	Slit 325

Applicants: Christopher C. Fraser (as amended) Serial No.: 09/766,511 Filed

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	_	9	
2870 CTGGTCC :::: GATCC 1120	2940 [GTGGAT	3010 ATAGTG : :	3080 AATTCA ::::: ATTCA 1190
2860 2870 GCTCGTTGTGCTGGTCC ::::. :::: CTTTGAAGATCC 1120	2930 GTCAAGGTCC1 ::::. GTCAT	3000 rggcacargra	3070 GTGATGTCCC
2850 .GCCTGGAATT(::: .GCAT	2920 29 AAATTTACCTGTCAA :.::::::	2990 GTAAAAATGAT : G	3060 GGGCAGGAC1 : TG
0 2840 28 TCGGAATATAAGGAGCCTG : :::::::::::::::::::::::::::::::::::	2910 TCCCTCCAAA	70 2980 GCCTATCAAATCCGTG' :::::::: GCCTTGCATCCAAG 50 1160	3050 ATGGTTTCAAGG ::::::
2830 GTGAAGTCGG : ::	2900 TACTCACAAC	2970 CCCCTGCCTA ::::	3040 ACCTGTCCAT:::TGTC
2820 ATCCGACTGG	2890 GATAAACTTT	2960 CTAAGTGTAA :. CA	3030 CTTTTACCGATGC ::::. -TTAAGCCGT
2810 2850 2870 2870 2850 2850 2850 2870 Slit ACATGCAGTGATGTGGTGAAGTCGGAATATAAGGAGCCTGGAATTGCTCGTTGTGCTGGTCC :::: 325 ACATTTGAAAATATGGGAGCATCTTTGAAGATCC 1090	2880 2930 2940 TGGAGAAATGGCAGATAAACTTTACTCACAACTCCCTCCC	2950 3000 3010 GTCAATATTCTAGCTAAGTGTAACCCCTGCCTATCAAATCCGTGTAAAAATGATGGCACATGTAATAGTG : ::::::::::::::::::::::::::::::::::	3020 3030 3040 3050 3060 3070 3080 ATCCAGTTGACTTTTACCGATGCACCTGTCCATTTCA ::: ::: ::: ::: :::::::::::::::::::::
slit 325 10	Slit 325	Slit 325	Slit 325

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3150 ATGGATTC	:: :: TGCAAAC 1230	3220 NGATAATG :	3290 AGTATAC	3360 TTCAAAG
3100 3110 3120 3130 3140 3150 CCATGTAAACATGGAGGAACTTGCCACTTAAAGGAAGGAGGAGAAGATGGATTC	::.:::::::::::::::::::::::::::::::::::	3210 ATGATTGTGAA	3280 TTGCCCACCTG :::: TTAC	3350 TGCCAGCACGA
3130 TTAAAGGAA	 	3200 TCAACGIIG :.::.	3270 CACATGCCTTTGC :: :::::: CAGCCATTAC 1270	30 3340 AGGACCTGAACCCCT :::::::GTCAGAATCCCC- 1290
3120 AACTTGCCAC	:: : ::: CTAATC-CTT- 1210	3190 AATTGTGAAG	3260 TTAATAACTACAC : :::: [CTTCA-	3330 IGCCCAGGACCT ::: ITGTCAG
3110 ACATGGAGG		3180 GAAGGAGA <i>A</i> /	3250 TCGATGGCATT ::::: TAGCAT- 1260	3320 GCTGGACTTCTGTGC ::.:::: TCTAAACATCTATT- 1280
3100 ACCCATGTAA	::. CAAATT-	3170 GATGGATTT	3240 CTACATGTG .:	3310 GGAGAAGCT
3090 TGCCTGCATCAGTAAC	: :::: TCTTCAGG	3160 3170 3180 3190 3200 3200 3220 TGGTGTATTTGTGATGGAGAAAATTGTGAAGTCAACGTTGATGATTGTGAAGATAATG : :::::::::::::::::::::::::::::::::::	3230 3240 3250 3260 3270 3280 3290 ACTGTGAAAATAATTCTACATGTCGATGGCATTAATAACTACACATGCCTTTGCCCACCTGAGTATAC :::: ACTGGCTAGCATCTTCAGCCATTAC	330 3340 3350 3360 AGGTGAGTTGTGAGGACTTCTGTGCCCAGGACCTGAACCCCTGCCAGCACGATTCAAAG ::::::::::::::::::::::::::::::::::
Slit	325	Slit 325	slit 325 12	slit 325

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	140p1460111611	is a square shoot	
3430 GACATCG	3500 GCTATAC ::: ATAA 1360	3570 TCGTACC . :. : AAGAC	3640 AGCCAATATGTC ::::::: CAA-ATGGC 1450
3420 FGAACACTGC	3490 GCAGTGAACG	3560 ATGGTCCTCCTCGT;::::::::::::::::::::::::::	3630 AATGAGCCAA ::: CAA 1450
3410 AGGGTACGTAGG1 ::::: TTACGTT	0 CCCACTGCACAGATG : :: :: -CATCTTCA	3540 3550 3560 35 TGAGTTTTCTCCACCCATGGTCCTCCTCGTA :::::::::::::::::::::::::::::::::	3620 ATCGTCAGAATA :.: :: AACCA
390 3400 TGTGACTGCACACCA :::::: -GTGGCAGAGCA 310	3470 AACGGAGCCC. :	3540 CTGTGAGTT :	3610 3620 AGCTCAGTGTATCGTCAG ::.:.:::: -GCATAAGTAACCA-
3390 CAAATGTGAC :::: GTGGC	3460 AAGTGTAAAA ::::: TTGTGTTA 1350	3530 ACAGTGGCTTGTTC :. ::: ::: -CTTGGGCT-GTT- 1380	3600 TCAGAATGGA ::: CCTG
3380 CAAAGGGATT	3450 3460 CCAAGACAAGTGTAAA : ::: .:::::-: ATTACAAATTGTGTTA- 1340 1350	3520 CCGAAGGTTACA :::: CCAGAGCT	3590 36 NTTTGATTGTCAGA : :: : :: NTGATGGCCTG- 1430
3370 3380 3400 3410 3420 3430 Slit TGCATCCTAACTCCAAATGTGACTGCACCAGGGTACGTGAACACTGCGACATCG ::::::::::::::::::::::::::::::::::::	3440 ATTTTGACGACTG :::::: ATATTAAC 1330	3510 3520 3530 3540 3550 3560 3570 GTGCATATGCCCCGAAGGTTACAGTGGTTCTTGTGAGTTTTCTCCACCCATGGTCCTCCTCGTACC :::::::::::::::::::::::::::::::::::	3580 3600 3610 3620 3630 3640 Slit AGCCCCTGTGATATTTTGATTGTCAGAATGGAGCTCAGTGTATCGTCAGAATAAATGAGCCAATATGTC : :::::::::::::::::::::::::::::::::
Slit 325	Slit 325	Slit 325	Slit 325

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3710 AAACAAAGAGTC	1500 3780 3780 CAGATGAA	.:.:. TGGTAA-	3850 CGTGTTC	:::. GCAAATAC 1590	3920 ATGGAAA : CT
3690 3700 37 TGTGAATTTTATAAACAAAGAG':::::::::::::::::::::::::::::	.CAILACIIICI 1490 1 3770 CAGATTGCCAC	::::::. .GAATGCCTTT 1550	3840 TATCGGGG	1	3910 STGGAGACAATCAATG ::::::::::-::: TGGAAAAAACAGTG 1630
3690 AGTGTGAATT ::::::	14 14 3760 PACACTICA	: .:.: TTTTCAAGA(3830 GTAGAACTC	::::::::::::::::::::::::::::::::::::::	3900 GTGTGGAGA ::::::
3660 3700 3680 3690 3700 3710 TCAGGGAGAAAAGTGTAAAAATTGGTTAGTGTGAATTTTATAAACAAAGAGTGTGTGAAATTGGTTAGTGTGAATTTTATAAACAAAGAGTGTGAAAAGTGAGAAGTGTGAAAAAATTGGTTAGTGAAATTTTATAAACAAAGAGTGTGAAAAAATTGGTTAGTTA	1470 1480 1490 1500 1500 1500 1500 1500 1500 1500 3730 3740 3750 3760 3770 3780 1CAGCCACAGACATAACACTTCAGATTGCCACAGATGAA	::::::::::::::::::::::::::::::::::::::	3820 CCATATCGCG		3870 3880 3890 3900 3910 3920 CGGCTCTCATCCAGCTTTTACAGTGTGGAGACAATCAATGATGGAAA : :: :: :: :: :: :: :: :: :: :: :: : : :
0 3670 3 GGGAGAAAGTGTGAAAA :::::::::::-::-	3740 3TCGGCCTC	:::: : : -TTCACCTGC 1520	3810 STGACAAAGA	3AGACTA 15	3880 rccagcrrcr : :: :: crrcrgrr/
3660 ATCAGGGAGA :::::	1470 3730 TTCAGCCAAGG	: . : TAC	00 TATAAGG	.::: .: TCCATTA(3870 CCGGCTCTCA1
325 AGTCCTCT-	460 3720 TTATCTTCAGATTCCT	::::: CGAATTCCT 1510	3790 GGAATCCTC	 IC	3860 GTGCCAGCTATGACAC ::: AA-CTTACTA
Slit AGTGT ::		325	Slit GACAG	325	3860 Slit GTGCCAGCTA :.:: 325 AA-CTTACTA 1600

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				-	
3990 CCCAAA	4060 TGCCAG	 	4130 ;carccg	4200 ccrggc	
3980 ATGGTGGGAAC :::::	4050 TGTAGGAGGCA		4120 TTCCACGGCTG :: TT	4190 CAGGCATTTTG	 TTTTAATCATTTT- 1760
3970 rcrrrgrccgrcc :::::	1660 4040 CTCTCCACTCTA	! ! ! ! ! !	4100 TGGGCAGAACGGAACCAGCTT:::::::::::::::::::	1/30 4180 CCGATGCAAA	1 1 2 1 1
3960 GAGTCTCTCT ::	16 16 4030 AATTTTGACT	::.:: ACACAAGAAGTIGA 1690	4100 CTGGGCAGAA : :::: -TTGACATTT	1/20 4170 CCAGAAGGTG	GTG- 1750
3950 CCTTGGATCA	4020 GTCCACTCTG	:::::. ACACAAGAAG 1690	4090 CGCCAGGCCC	4160 TGCAGGACTT	T.T
3940 GAACTACTTG :.:.	1650 4010 TTGTCAAAGCA	:::: TTGT	4080 GTGGCATCTCTG ::::: GAGGCTT	4150 AACAGTGAGC	T
3980 3990 3990 3960 3960 3970 3980 3990 3990 3990 3990 3990 3990 399	_	::::::::::::::::::::::::::::::::::::::	4070 AAGAGTAAC ::::: AAGTTGAAT	1/30 1/30 4140 4150 4160 4170 4180 4190 4200 Slit GAACCTTTACATCAAGTGAGCTGCAGGACTTCCAGAAGGTGCCGATGCAAACAGGCATTTTGCCTGGC	325TTTTCATC-

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	replacemen	a rigure sheet	
4270 TTCACCT :. TAA 0	30 4340 CCTTGGAAATAA ::::::-:- -CAAGGGAAAAT 820	4410 GCCATGGA :::: ATGTA 1870	4480 GGGAAGT .:.::: AGAAAGT
4260 CAGGCAGGCTT ::::::	4330 CTTGCCTTG :.: CAAG	4400 TTGGAGGG	460 4470 4480 GATCAAGTGCAAGCACGGGAAGT ::::::::-::::::::::::::::::::::::::::
4250 AGCCCAGCAGCC	4320 SACCAATGACCO	4380 4390 GTTCTCCTACAGCTGTAAGTGC :: :: .: .: .: .: .:	4460 AGGCGATCAAGT ::::: CAAAT 1900
4240 GGCACATGCC?	00 4310 CCTCTGTGACCAACG(: :::::::::::::::::::::::::::::::::::	4380 GCGTTCTCCTACAG ::::::: TTATCAGTCAG 1850	4450 TTAACCCATGCCA ::::::::: -TAACACTTCCC- 890
4230 TGTGTGCCCAT ::: TGTT	4300 GGGCCCCTCT :::: CATCA	4370 CCATCAATGC	4440 GGATCTGTTTA :: TA 1890
4220 ACAAGAAGGTGTG .:: ::: AAAGTTGTT 1780	4290 AAGGATGGATG:::: AAGG	4360 ACCTGCTTGC :::::: FACAGCTT	4430 ATGAAGAGGA(::
4210 4220 4230 4240 4250 4260 4270 Slit TGTGAGCCATGCCACAGGTGTGTGCCCATGCCACCCAGCCCAGCCAG	4280 4290 4310 4320 4330 4340 GCGAGTGCCAGGATGGATGGGCCCCTCTGTGACCAACGGACCAATGACCTTGCCTTGGAAATAA .::::::::::::::::::::::::::::::	4350 4360 4410 Slit ATGCGTACATGCCACCTGCCATCAATGCGTTCTCCTACAGCTGTAAGTGCTTGGAGGGCCATGGA : :: :: :: :: :: :: :: :: :: :: :: :: :	4420 4430 4440 4450 4460 4470 4480 GGTGTCCTCTGTGAAGAGGATCTGTTTAACCCATGCCAGGCGATCAAGTGCAAGCACGGAAGT :::::::::::::::::::::::::::::::::
Slit 325	Slit 325	Slit A' 325 A(1830	Slit 325

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	•	O	
4550 GTGATCG :.:.:.	4620 TTGCCAA ::: :: TTGA	4690 CCGCTGA : : ACTC	4760 AGAAAGT :.: AAA
4540 4550 GGGACAGCTGTGATCG ::: : ::::	0 CAGGGCTATGCTGC :::::::: CAGGTC-ATTCTTT 1980	4680 GGTGTGGACCGC::::::::::::::::::::::::::::	4750 4 TGGACGAGGTTGAGAA ::::::::::: TGGACATGATTTAAA- 2050
500 4510 4520 4530 4540 4550 GGGCAGCCCTACTGTGAATGCAGCAGTGGATACACGGGGGACAGCTGTGATCG :.::: GAGCAGCAGCCCTACTGTAATGCAGCAGCAGTTGATCG :.::: 1930	4600 4610 4 AAGCAGGGCTATGCTGCTTGC ::::::::::::GCA-CAGGTC-ATTCTTTTG- 1970 1980	640 4650 4660 4670 4680 4690 CCGATTAGAGTGCAGGGGTGTGCAGGAGGGCAGTGCTGTGGACCGCTGA ::::::::::::::::::::::::::::::::::::	4740 CCTTTG
4520 ATGCAGCAG1 	4590 TATTACCAAA	4660 GTGGGTGTGC	4730 TGACGGCTCCT .:.: ::. TCAGTGCCA
4510 CCTACTGTGA	4580 AAGGATAAGAGAT .:.:.:: -TGAAAATGAG	4650 3AGTGCAGAG	710 4720 TACTCTTTCGAATGCAC:::::::::::::::::::::::
4500 TCTGGGGCAGC(::::: GGAGCAG 1930	4570 CGAGGGGAAAGG : :TGA 1960	4640 TGTCCCGATTA(4710 GAAATACTCTT: :.:. :::: -ATATTGTCTA: 2020
4490 4 Slit GCAGGCTTTCAGGTCTG :::::: 325 CCTGGCTTG 1920	4560 4570 4580 4590 4600 4610 4620 Slit AGAAATCTCTTGTCGAGGGAAAGGATAAGAGTTATTACCAAAAGCAGCGGGCTATGCTGCTTGCCAA :: :: :: :: :: :: :: :: :: :: :: :: :	4630 4 Slit ACAACCAAGAAGGTGTC ::::: 325 ACATTC	4700 GGAGCAAGCGGCG :.:.: AACTAA
Slit 325	Sli 32	Sli 32	Slit 325

Fig. 2H-1'

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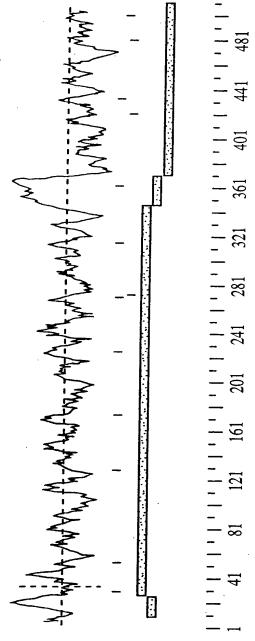
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4830 AAGGTTĞ	 ATATAATTA 70	4900 AAAATAC ::: TAA		
4820 GTCTTTGGAA	::: ::::::::::::::::::::::::::::::::::	4890 AATATATTGT. ::::::::: AATATGTTTT		
4810 CGGCAGCTCT	 - - - - - -	4870 4880 4890 TTCATAGTGGAAATATTTGAAATATATT : : . : : : : : : : : : : : : :	4950 GCATTTG ::	
4780 4790 4800 4810 4820 4830 ACGAGGIGIGICTITGGAAAAGGITG	::: ::: AAACCTC- 2060	4870 CTTCATAGTGG :::. ATATGAGGTTP	4920 4930 4940 4950 TATTATGAGAATAAGACTTTTTTTCTGCATTTG .:.:::::::::::::::::::::::::::::::	Fig. 2H-18
4790 TGTGTGTCCT	:: AAZ 2060	850 4860 TGGGACTAATGAATG:::::: GAAATATAATGAATT	4920 4930 TATTATGAGAATAAAGACTT'	5
4780 CTGTACGAGG	::: CTG	4850 CCATGTGGGA :: TGGAAAT. 2090	4920 TATTTTTTTTTTT::::::: :::::::::::::::::	
4770 Slit GGTGAAGTGCGGCTGT		4840 4850 4860 4870 4880 4890 4900 TATACTTCTTGACCATGTGGGACTAATGAATGCTTCATAGTGGAAATATTTGAAATATTGTAAAATAC :::::::::::::::::::::::::::::::	4910 Slit AGAACAGACTTATTTT':::325TAAAAA	
Slit	325	Slit 325 225	Slit 325	

Applicants: Christopher C. Fraser (as amended)
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RV 70	1	R O	J J O	N " N C
VGQVAWAR		FPAGSFQAR 140	20 AAVTSEFHL :::::::: AAVTSEFHL 210	90 SEGQPPPSY ::::::::: SEGQPPPSY 280
FYRGDSGEQ 60	 	SEYECRVST 130	10 20 -KGTTSSRSFKHSRSAAVTSEFHL ::::::::::::::::::::::::::::::::::::	80 KEGAMLKCL :::::::: KEGAMLKCL
7LGQDAKLPC: 50	! ! ! ! !	LRNAVQADEC 120	KGTTS: ::::: DTEVKGTTS: 190	70 EDQNLWHIGH :::::::: EDQNLWHIGH 260
LETSDVVTVV	! ! ! ! !	PRNPLDGSVI 110	 EGSPAPSVTW 180	60 FLAEASVRGL ::::::::: FLAEASVRGL 250
LLLLLLASFTGRCPAGELETSDVVTVVLGQDAKLPCFYRGDSGEQVGQVAWARV 20 30 40 50 60 70	! ! ! ! !	YEGRVEQPPP 100		0 80 HPGLLQDQRITHILHVSFLAEASVRGLEDQNLWHIGREGAMLKCLSEGQ ::::::::::::::::::::::::::::::::::::
AWLLLLLLLA 20	 	SKYGLHVSPA 90	 IBGPALEEGQ	40 WSHPGLLQDO :::::::: WSHPGLLQDO 230
MPLSLGAEMWGPEAWL 10		DAGEGAQELALLHSKYGLHVSPAYEGRVEQPPPRNPLDGSVLLRNAVQADEGEYECRVSTFPAGSFQAR 80 130 140	10 20	30 40 50 70 90 ALT VPSRSMNGQPLTCVVSHPGLLQDQRITHILHVSFLAEASVRGLEDQNLWHIGREGAMLKCLSEGQPPPSY ::::::::::::::::::::::::::::::::::
T364	ALT	T364	ALT T364	ALT T364

Applicants: Christopher C. Fraser (as amended) Serial No.: 09/766,511 Filed Filed: January 19, 2001

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uses thereof (as amended)

Atty/Agent: Mario Cloutier

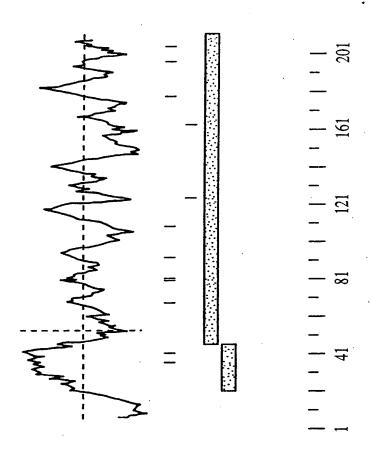
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ALT	100 NWTRLDG	o 3PLPSGV.	110 RVDGDTLGFP	120 PLTTEHSGI	130 YVCHVSNEFS	140 SRDSQVTVDV	100 110 120 130 140 150 160 160 ALT NWTRLDGPLPSGVRVDGDTLGFPPLTTEHSGIYVCHVSNEFSSRDSQVTVDVLADPQEDSGKQVDLVSAS	160 VDLVSAS
T364	::::: NWTRLD	3PLPSGV	RVDGDTLGFP	PLTTEHSGI	YVCHVSNEFS	SRDSQVTVDV	T364 NWTRLDGPLPSGVRVDGDTLGFPPLTTEHSGIYVCHVSNEFSSRDSQVTVDVL-DPQEDSGKQVDLVSAS	::::::
·	170	0 7 0	300	310	320	330	340	
ALT	VVVVGV	IAALLFC	TLVVVVVLMS	RYHRRKAQQI	MTQKYEEELT:::::::	VVVVGVIAALLFCLLVVVVVLMSRYHRRKAQQMTQKYEEELTLTRENSIRRLHSHHTDPRSQ ::::::::::::::::::::::::::::::::::::	ALT WWWGVIAALLFCLLWWWWLMSRYHRRKAQQMTQKYEEELTLTRENSIRRLHSHHTDPRSQ-	; ; ; ; ;
T364	4 VVVVGV.	IAALLFC 360	LLVVVVVLMS 370	RYHRRKAQQI 380	MTQKYEEELT 390	LTRENSIRRL 400	T364 VVVVGVIAALLFCLLVVVVVLMSRYHRRKAQQMTQKYEEELTLTRENSIRRLHSHHTDPRSQPEESVGLR 350 360 370 380 390 410	EESVGLR
			230	240	250	260	270	
ALT	1 1 1	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	SEEPEG	RSYSTLTTVI	REIETQTELL	SPGSGRAEEE	-SEEPEGRSYSTLTTVREIETQTELLSPGSGRAEEEEDQDEGIKQAMNHFVQEN	NHFVQEN
T364	AEGHPD(SLKDNSS	::::: CSVMSEEPEG	RSYSTLTTV	::::::::::::::::::::::::::::::::::::::	SPGSGRAEEE	T364 AEGHPDSLKDNSSCSVMSEEPEGRSYSTLTTVREIETQTELLSPGSGRAEEEEDQDEGIKOAMNHFVOEN	:::::: NHFVOEN
4	420	430	440	450	460	470	480	N.
	280	290						
ALT	GTLRAKI	PTGNGIY	ALT GTLRAKPTGNGIYINGRGHLV					
	••	•••						
T364	GTLRAKI	PTGNGIY	T364 GTLRAKPTGNGIYINGRGHLV					
4	490	200	510					

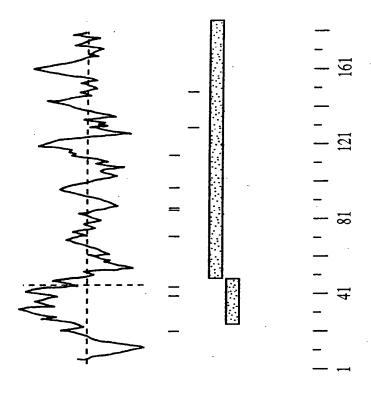
Applicants: Christopher C. Fraser (as amended)
Serial No.: 09/766,511 Filed: January 19, 2001
Title: Nucleic acids encoding Tango 405 and functional fragments and uses thereof (as amended)
Atty/Agent: Mario Cloutier
Attorney Docket No.: MPI00-537OMNIRCEM

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Applicants: Christopher C. Fraser (as amended)
Serial No.: 09/766,511 Filed: January 19, 2001
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Atty/Agent: Mario Cloutier
Attorney Docket No.: MPI00-537OMNIRCEM

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Serial No.: 09/766,511 Filed: January 19, 2001
Title: Nucleic acids encoding Tango 405 and functional fragments and

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			opinione rigure sheet 33 01	39
70	CFSEG	CFSEG	FSYFL .::: LSYFL MNKIY	
09	SLRLWSVAGISIALLSACFIVSCVVTYHFTYGETGKRLSELHSYHSSLTCFSEG	.:::::::::::::::::::::::::::::::::::::	90 100 110 120 130 SFGSSCYFISSEEKVWSKSEQNCVEMGAHLVVFNTEAEQNFIVQQLNESFSYFL :::::::::::::::::::::::::::::::::::	
50	FTYGETGKRL	: FIMDQPSRRL 50	120 ::::::::::::::::::::::::::::::::::::	
40	IVSCVVTYH	:.::::: IASCVVTYQ 40	100 110 12 KVWSKSEQNCVEMGAHLVVFNT .:::::::::::::::::::::::::::::::::::	
30	ISIALLSACE	::.:::: ISMLLLSTCF 30	90 100 FGSSCYFISSEEKVWSKS :::::::::::::::::::::::::::::::::::	
20	WLSLRLWSVAG	: .::::: W-TLRLWSAAV: 20	90 ::::::::::::::::::::::::::::::::::::	
10	human MMQEQQPQSTEKRGWL	::::::: murine MVQERQSQGKGVC-W-	80 90 110 120 130 130 130 130 140 150 150 150 150 150 150 150 150 150 150 150 150 170 180 190 200 100 100 140 150 160 170 180 190 200 100 140 150	
	human 1	murine N	human TK murine TM 70 human GL ::	

Fig. 4

rine O

Title: Nucleic acids encoding Tango 405 and functional fragments and uses thereof (as amended)

Atty/Agent: Mario Cloutier

Attorney Docket No. 2 Appears

Attorney Docket No.: MPI00-537OMNIRCEM

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		1	igure sheet 34 (Л 39
70 TGTGG	AGCTG	140 ACATA : ATTAT 0	210 AAGGG ::::: AAGGG	CTACT
60 GACTCTGGTC	::::::::::::::::::::::::::::::::::::::	110 120 130 TTCATTGTGAGCTGTAGTAACTTACCATTTTA ::::::::::::::::::::::::::::::::	160 170 180 190 200 21 AGGCTGTCTGAACTACATATCATTCAAGTCTCACCTGCTTCAGTGAAGG ::.:::::::::::::::::::::::::::::::	230 240 250 260 270 TGGGGATGTTGCCCAGCTTCTTGGAAGTCATTTGGTTCCAGTTGCTACT ::::::::::::::::::::::::::::::::::
50 TGTCCCTGA	GGACCCTGA	120 TGTAGTAACT' :::.::: TGTGGTGACT'	190 AGTCTCACCT:::::	250 260 TGGAAGTCATTTGG ::::::::: TGGAAGTCATTTGG
40 GAGGCTGGT	::: ::: : : : : : : : : : : : : : : :	110 TGTGAGCTG: :: ::::: TGCGAGCTG'	180 .TATCATTCA :::::: .TACCATTCC 180	250 CTTCTTGGA : ::: ATCACTGGA 250
30 CAGAGAAAA	:::::- -AGGGAAGG 30	100 CTTGCTTCAT::::: CCTGTTTCAT	170 ACTACACTCA:::::: ACTTCACACA:	240 GTTGCCCAGC : ::::. GCTGCCCAAP
O CTCAAAGTA	: :: 3CCA	100 CCTCAGTGCTTGC : ::::::	CTGTCTGAA	230 TGGGGATGT :::::: :GTGGGGATGC
20 GCAGCAACC	::: : AAGACAATCC 20	90 ATTGCACTCC :: ::: ATGTTACTCT 80	160 :GCAAAAGGC : : : : : : : : : : : : : : : : : : :	CAGCC ::: CAGAAAAAA 220
10 20 40 50 50 human ATGATGCAAGGAACCTCAAAGTACAGAGAAAAAAGAGGCTGGTTGTCCCTGAGACTCTGGTCTGTGTGG	::::::::::::::::::::::::::::::::::::::	80 100 110 120 130 140 CTGGGATTTCCATTGCACTCCTCAGTGCTTGCTTCATTGTGAGCTGTGTAACTTACCATTTTACATA ::::::::::::::::::::	150 160 200 210 human TGGTGAAACTGGCAAAAGGCTGTCTGAACTACACTCATTCAAGTCTCACCTGCTTCAGTGAAGGG : : : : : : : : : : : : : : : : : :	220 ACAAAGGTGC ::.:.:: ACTATGGTGT
human	murine	human murine	human murine	human murine

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		Replacement 1	rigure sheet 33 (UI 37
340 CATTTGGT	::: :::: CATCTGGT 340	410 ATTTTCTG : :: :: ACTTCCTG 410	480 AAAATGTCA :::::::: AAAATGTCA 480	550 AAACCTAC
330 BAGATGGGAGCA	::::::::::::::::::::::::::::::::::::::	400 GTCATTTTCTT :::::::::::	470 CCTTATGAGAA ::::. :: CCTTTCAGTCA 470	540 TAGTCTTCTGG
300 340 320 330 340 GAAGGTTTGGTTTGAGATGGGAGCACATTTGGT	::: ::::::::::::::::::::::::::::::::::	350 360 370 380 390 400 410 TGTGTTCAACACAGAAGCAGAATTTCATTGTCCAGCAGCTGAATGAGTCATTTTCTTATTTTCTG ::::::::::::::::::::::::::::::::	420 430 440 450 460 470 480 GGGCTTTCAGACCCCACAAGGTAATAATTGGCAATGGATTGATAAGACACCTTATGAGAAAATGTCA ::::::::::::::::::::::::::::::::::::	490 500 510 520 530 540 550 human GATTTTGGCACCTAGGTGAGCCAATCATTCTGCAGAGCAATGTGCTTCAATAGTCTTCTGGAAACCTAC :::::::::::::::::::::::::::::::
310 TAAGAGTGAGC	: ::::: caccagrgagcz 310	380 TTCATTGTCCA(:::: . ::: TTCATCACCCA(380	450 ATTGGCAATGGZ :.::::::: AATGGCAATGGZ	0 510 520 53 GTGAGCCCAATCATTCTGCAGAGCAATGTG .::::::::::::::::::::::::::::::::::
300 GGTTTGGTC	:::: CTTCTGGAG	370 5AGCAGAAT ::::::: 5AGCAGAAT	440 STAATAATAA :::::::: STAATGGCAA	510 SCCCAATCAT :::::::
290 TGAAGAGAA	.:.::: CAAGGAGAAC 290	360 ACAGAAGCAC :::::::: ACTGAAGCGC	430 ACCCACAAGG : ::::: ATCC-CAAGG	500 ccraggrgag :: .::. ccccargaz 500
280 human TCATTTCCAGTGAAGA	::::::: TCATTTCTACCAAGGA 280 290	350 TGTGTTCAACACAGAA :::::::::: GGTGATCAATACTGAA 350	420 GGGCTTTCAG :: ::::: GGTCTTTCGG	490 GATTTTGGCACC' :.:: ::::: GGTTCTGGCACC
human	murine	human murine	human murine	human murine

Fig. 4E

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Fig. 4F

human CTA

Applicants: Christopher C. Fraser (as amended)
Serial No.: 09/766,511 Filed: January 19, 2001
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Atty/Agent: Mario Cloutier
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### ### ##############################				_				_	_						
### ##################################		FSEGTM	FSEGTM	70	140	SYFLGL	•••	SYFLGL	T 4 0		SGVFQ	:	KKIYL		
mT405 MVQERQSQGKGVCWTLRLWSAAVISMLLLSTCFIASCVVTYQFIMDQPSRRLYELHT :::::::::::::::::::::::::::::::::::)	YHSSLTC	YHSSLTC	09	130	QQLNESL	•••	COLNESL) T ? ()		QK	•	HNSICEM	200	
mT405 MVQERQSQGKGVCWTLRLWSAAVISMLLLSTCFIASCVVTYQFIMDQPSRRL :::::::::::::::::::::::::::::::::::		YELHT	YELHT		•	ONFIT(•••	ONFIT	•		 	••	FCDSKI		
mT405 MVQERQSQGKGVCWTLRLWSAAVISMLLLSTCFIASCVVTYQFIMDG :::::::::::::::::::::::::::::::::::		DPSRRL'	PSRRL.	20	120	INTEAE	•••	INTEAE	071	170	I	•	MGWNDV	190	
mT405 MVQERQSQGKGVCWTLRLWSAAVISMLLLSTCFIASCVVTY 10 20 30 40 80 90 100 110 mT405 VSEKMWGCCPNHWKSFGSSCYLISTKENFWSTSEQNCVQMG 110 150 160 mT405 SDPKVMANGNGSMILLSVKMSGSGTPMNP Dectin SDPQGNGKWQWIDDTPFSQNVRFWHPHEPNLPEERCVSIVY 150 160 170 180 Fig. 4G		QFIMDO	QFIMDO			AHLVV	•••	AHLVV.			1 1 1		WNPSKI		
mT405 MVQERQSQGKGVCWTLRLWSAAVISMLLLSTCFIAA ::::::::::::::::::::::::::::::::::	1	SCVVTY	SCVVTY	40	110	NCVQMG	•••	NCVQMG.) 		1		CVSIVY	180	. 4G
mT405 MVQERQSQGKGVCWTLRLWSAAVISMLLLS :::::::::::::::::::::::::::::::::		TCFIA	TCFIA			STSEQ	•••	STSEQI			NP	••	LPEER(Fig
mT405 MVQERQSQGKGVCWTLRLWSAAVI: :::::::::::::::::::::::::::::::::		SMLLLS	SMLLLS	30	100	TKENFW	••	TKENFW	- - -		GSGTPM	••	HPHEPN	170	
mT405 MVQERQSQGKGVCWTLRLW :::::::::::::::::::::::::::::::::::		SAAVI	SAAVI	0	06	CYLIS	••	CYLIS	2	160	SVKMS.		NVRFW	0.0	
mT405 MVQERQSQGKGVCU ::::::::::::::::::::::::::::::::::::		WTLRLW	WTLRLV	(1	01	KSFGSS	•••	KSFGSS	, ,		SSMILI	•	DTPFS	16	
mT405 MVQERQSÇ ::::::: Dectin MVQERQSC ::::::: Dectin VSEKMWGC mT405 SDPKVMAN :::: Dectin SDPQGNGF		GKGVCI	GKGVCI	10	80	CPNHW	••	CPNHW	0	150	IGN(•	MOMID	.50	
mT405 MV(:: Dectin MV(:: Dectin VSI mT405 SDI :: Dectin SDI		QERQSÇ	QERQSQ			EKMWGC	•••	EKMWGC			PKVMAN	•	PQGNGK	r- -1	
mT40 mT40 mT40 mT40		5 MV(n MV(5 VSI	••				5 SD	••	n SDI		
		mT40	Decti			mT40.		Decti			mT40;		Decti		

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			Fig. 4H) personal			
CEMKKIYL	:::::: VFCDSKHNSI 200	::::::::::::::::::::::::::::::::::::::	: .: .: :: .: .: .: .: .: .:	::: WHPHEPNI 170	::. ::::::::::::::::::::::::::::::::::	GLSDPQGNGKWQWIDDTPFSQNVRFWHPHEPNLPEERCVSIVYWNPSKWGWNDVFCDSKHNSICEMKKIYL 150 160 170 170 180	Dectin
CEMNKIYL	200 VICETRRNSI	190 WKPTGWGWND	180 HSAEQCASIVF	170 WHLGEPNI	160 IDKTPYEKNVRF	150 160 170 180 190 200 hT405 GLSDPQGNNNWQWIDKTPYEKNVRFWHLGEPNHSAEQCASIVFWKPTGWGWNDVICETRRNSICEMNKIYL	hT405
::::: ESLSYFL 140	::::::::::::::::::::::::::::::::::::::	::::::::::::::::::::::::::::::::::::::	SFGSSCYLISTKENFWSTSEQNCVQMGAHLVVINTEAEQNFITQQLNESLSYF 90 100 100 110 120	STKENFW	HWKSFGSSCYLI 90		Dectin
140 ESFSYFL	130 EQNFIVQQLN	120 AHLVVFNTEAI	110 SKSEQNCVEMG	100 SSEEKVW	90 SWKSFGSSCYFI	80 90 100 110 120 140 hT405 TKVPAWGCCPASWKSFGSSCYFISSEEKVWSKSEQNCVEMGAHLVVFNTEAEQNFIVQQLNESFSYFL	hT405
LICESEG 70	LYELHTYHSS 60	QFIMDQPSRR] 50	TLRLWSAAVISMLLLSTCFIASCVVTYQFIMDQPSRRLYELHTYHSSLTCFSEG 20 50 60 70	ISMLLLS: 30	-W-TLRLWSAAV 20	ectin MVQERQSQGKGVC-W-)ectin
LTCFSEG	LSELHSYHSS	HFTYGETGKRI	ACFIVSCVVTY	ISIALLS	GWLSLRLWSVAG	hT405 MMQEQQPQSTEKRGWLSLRLWSVAGISIALLSACFIVSCVVTYHFTYGETGKRLSELHSYHSSLTCFSEG	hT405
70	0.9	50	40	30	20	10	

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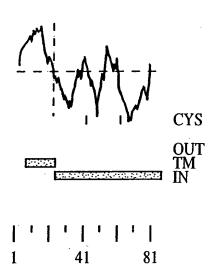


Fig. 5A